

Brannock, Michael

From: Brannock, Michael
Sent: Wednesday, August 02, 2006 12:01 PM
To: STIC-Biotech/ChemLib
Subject: 10622373

Please provide a full length search of SEQ ID NO: 1 and a full length and oligo search of SEQ ID NO: 2 against commercial, issued, and published sequence databases.

Thank you

Michael T. Brannock, Ph.D.
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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:28:53 ; Search time 205 Seconds
(without alignments)
3172.457 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 1404
Sequence: 1 YWTFPVCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1404	100.0	1404	4	US-10-622-373-2
2	1404	100.0	1404	5	US-10-756-149-5141
3	60	4.3	60	4	US-10-639-067-156
4	57	4.1	225	4	US-10-108-260A-2706
5	57	4.1	655	4	US-10-108-260A-3501
6	57	4.1	838	4	US-10-622-373-6
7	54	3.8	54	4	US-10-639-067-157
8	50	3.6	50	5	US-10-776-013-606
9	50	3.6	50	5	US-10-776-013-607
10	44	3.1	44	4	US-10-639-067-155
11	34	2.4	34	4	US-10-764-425-138
12	20	1.4	20	5	US-10-776-013-601
13	20	1.4	20	5	US-10-776-013-602
14	20	1.4	20	5	US-10-776-013-603
15	20	1.4	20	5	US-10-776-013-604
16	20	1.4	20	5	US-10-776-013-605
17	16	1.1	74	3	US-09-864-761-35325
18	15	1.1	339	4	US-10-264-049-2738
19	13	0.9	177	4	US-10-104-047-3332
20	13	0.9	177	6	US-11-072-512-3332
21	10	0.7	23	5	US-10-862-195-708
22	9	0.6	265	4	US-10-398-037-15
23	8	0.6	84	4	US-10-424-599-223494
24	8	0.6	97	5	US-10-450-763-48794
25	8	0.6	99	3	US-09-925-297-842
26	8	0.6	113	4	US-10-767-701-47115
27	8	0.6	114	3	US-09-978-360A-726
28	8	0.6	114	3	US-09-978-360A-726
29	8	0.6	114	4	US-10-319-763-214
30	8	0.6	115	4	US-10-319-763-120
31	8	0.6	125	4	US-10-425-115-223773

32	8	0.6	185	4	US-10-425-114-48958	Sequence 48958, A
33	8	0.6	217	4	US-10-424-599-217689	Sequence 217689,
34	8	0.6	320	4	US-10-084-846A-84	Sequence 84, Appl
35	8	0.6	320	6	US-11-087-099-9834	Sequence 9834, Ap
36	8	0.6	397	4	US-10-767-701-45226	Sequence 45226, A
37	8	0.6	429	4	US-10-369-493-21679	Sequence 21679, A
38	8	0.6	433	4	US-10-369-493-20299	Sequence 20299, A
39	8	0.6	445	5	US-10-732-923-4200	Sequence 4200, Ap
40	8	0.6	447	4	US-10-424-599-250782	Sequence 250782,
41	8	0.6	454	4	US-10-369-493-8687	Sequence 8687, Ap
42	8	0.6	460	3	US-09-864-761-43042	Sequence 43042, A
43	8	0.6	469	4	US-10-369-493-22836	Sequence 22836, A
44	8	0.6	695	4	US-10-369-493-19882	Sequence 19882, A
45	8	0.6	888	4	US-10-282-122A-57155	Sequence 57155, A

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:02:28 ; Search time 209 Seconds
(without alignments)
3071.444 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVVTCTMTGAEIESGAQ.....AKELGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	7438	100.0	1404	8 ADJ57552	Adj57552 Human GAS
2	7380	99.2	1395	9 AEA23889	Aea23889 Human PRO
3	2084.5	28.0	838	4 AAM79102	Aam79102 Human pro
4	2084.5	28.0	838	8 ADJ57556	Adj57556 Human GAS
5	2077.5	27.9	838	8 ADQ66022	Adq66022 Novel hum
6	1794.5	24.1	901	4 AAM80086	Aam80086 Human pro
7	1794.5	24.1	901	7 ADC32958	Adc32958 Human nov
8	1677.5	22.6	635	5 ABB08788	Abb08788 Human LAM
9	1527.5	20.5	655	7 ADM04816	Adm04816 Human pro
10	1527.5	20.5	655	9 AEC87746	Aec87746 Human cDN
11	943	12.7	225	7 ADM04021	Adm04021 Human pro
12	943	12.7	225	9 AEC86951	Aec86951 Human cDN
13	896	12.0	2338	8 ABO58348	Abo58348 Human gen
14	732.5	9.8	2367	4 AAU31850	Aau31850 Novel hum
15	722.5	9.7	339	5 ABP41606	Abp41606 Human ova
16	720.5	9.7	574	4 ABG07996	Abg07996 Novel hum
17	682.5	9.2	570	7 ADJ69585	Adj69585 Human hea
18	674.5	9.1	547	6 ABR44353	Abr44353 Human lar
19	674.5	9.1	547	7 ADC31273	Adc31273 Human nov
20	674.5	9.1	547	7 ADC33434	Adc33434 Human p60
21	652.5	8.8	539	7 ADC33432	Adc33432 Rat p60TR
22	630.5	8.5	177	7 ADB65178	Adb65178 Human pro
23	625.5	8.4	176	9 ADV77071	Adv77071 Huntingto
24	550.5	7.4	558	3 AAB42722	Aab42722 Human ORF
25	550.5	7.4	558	4 AAB95263	Aab95263 Human pro
26	550.5	7.4	558	5 ABP69780	Abp69780 Human pol
27	550.5	7.4	558	5 ABB75717	Abb75717 Human cel

28	529	7.1	122	5	ABP07806	Abp07806	Human	ORF
29	473	6.4	310	9	AEA20290	Aea20290	Novel	hum
30	454	6.1	387	7	ADI60400	Adi60400	Secreted	
31	454	6.1	387	9	AEA21102	Aea21102	Novel	hum
32	444.5	6.0	367	7	ADI60171	Adi60171	Secreted	
33	360	4.8	453	4	AAM93332	Aam93332	Human	pol
34	360	4.8	453	4	AAG67208	Aag67208	Amino	aci
35	360	4.8	453	4	AAU28175	Aau28175	Novel	hum
36	360	4.8	453	4	AAG67135	Aag67135	Amino	aci
37	360	4.8	453	8	ADL30830	Adl30830	Human	pro
38	349.5	4.7	379	2	AAY17220	Aay17220	Human	sec
39	349.5	4.7	379	4	AAU38990	Aau38990	Human	sec
40	349.5	4.7	379	5	ABB55699	Abb55699	Human	pol
41	349.5	4.7	379	9	ADW09091	Adw09091	Human	sec
42	345	4.6	264	3	AAB32088	Aab32088	Human	sec
43	345	4.6	337	4	AAG67776	Aag67776	Amino	aci
44	345	4.6	342	4	AAB27240	Aab27240	Human	EXM
45	345	4.6	342	7	ADJ69028	Adj69028	Human	hea

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:12:27 ; Search time 56 Seconds
(without alignments)
2194.518 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVVTCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	630.5	8.5	177	2	US-10-104-047-3332 Sequence 3332, Ap
2	345	4.6	337	2	US-09-780-996A-9 Sequence 9, Appli
3	345	4.6	337	2	US-10-726-721A-9 Sequence 9, Appli
4	345	4.6	379	2	US-09-193-266-1 Sequence 1, Appli
5	284	3.8	1070	2	US-09-902-540-13861 Sequence 13861, A
6	245	3.3	1805	1	US-07-853-913-2 Sequence 2, Appli
7	221.5	3.0	1858	2	US-09-902-540-12643 Sequence 12643, A
8	221	3.0	1091	2	US-09-949-016-8595 Sequence 8595, Ap
9	217	2.9	1088	2	US-09-130-242-2 Sequence 2, Appli
10	217	2.9	1088	2	US-09-583-610D-2 Sequence 2, Appli
11	217	2.9	1088	2	US-09-949-016-6935 Sequence 6935, Ap
12	213.5	2.9	2476	2	US-09-824-574-7 Sequence 7, Appli
13	210.5	2.8	1781	2	US-09-961-403-13 Sequence 13, Appl
14	206	2.8	1780	1	US-08-769-309A-5 Sequence 5, Appli
15	206	2.8	1780	2	US-08-994-570-5 Sequence 5, Appli
16	202	2.7	1618	1	US-07-853-913-4 Sequence 4, Appli
17	202	2.7	1618	2	US-09-538-092-1143 Sequence 1143, Ap
18	202	2.7	1618	2	US-09-731-255-2 Sequence 2, Appli
19	202	2.7	1618	2	US-10-136-891-2 Sequence 2, Appli
20	196	2.6	2375	2	US-09-538-092-1131 Sequence 1131, Ap
21	194	2.6	674	2	US-08-893-852A-1 Sequence 1, Appli
22	193.5	2.6	1596	2	US-08-978-277A-4 Sequence 4, Appli
23	192.5	2.6	203	2	US-10-094-749-1808 Sequence 1808, Ap
24	190.5	2.6	1020	2	US-09-538-092-911 Sequence 911, App
25	188	2.5	3924	2	US-09-538-092-1246 Sequence 1246, Ap
26	184.5	2.5	1018	1	US-08-072-610-2 Sequence 2, Appli
27	184.5	2.5	1018	1	US-08-719-822B-2 Sequence 2, Appli
28	184.5	2.5	1018	2	US-09-092-458-2 Sequence 2, Appli
29	184.5	2.5	1018	2	US-08-719-821C-2 Sequence 2, Appli
30	181.5	2.4	1444	2	US-09-949-016-9652 Sequence 9652, Ap

31	181.5	2.4	2004	2	US-09-538-092-1371	Sequence 1371, Ap
32	181.5	2.4	2004	2	US-09-949-016-6756	Sequence 6756, Ap
33	181	2.4	901	2	US-09-248-796A-14747	Sequence 14747, A
34	181	2.4	1346	1	US-08-635-121-2	Sequence 2, Appli
35	181	2.4	1346	2	US-08-978-277A-2	Sequence 2, Appli
36	180.5	2.4	793	2	US-09-538-092-1271	Sequence 1271, Ap
37	176	2.4	1786	2	US-08-973-462-8	Sequence 8, Appli
38	172.5	2.3	1878	2	US-09-949-016-8902	Sequence 8902, Ap
39	172.5	2.3	1878	2	US-09-949-016-8903	Sequence 8903, Ap
40	171.5	2.3	3224	1	US-08-705-660-34	Sequence 34, Appl
41	171.5	2.3	3224	2	US-08-989-045-34	Sequence 34, Appl
42	171.5	2.3	3224	2	US-09-538-092-1161	Sequence 1161, Ap
43	171.5	2.3	3224	2	US-09-315-355A-34	Sequence 34, Appl
44	168	2.3	706	2	US-10-104-047-3843	Sequence 3843, Ap
45	168	2.3	2079	2	US-09-949-016-8301	Sequence 8301, Ap

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:13:22 ; Search time 205 Seconds
(without alignments)
3172.457 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVVTCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	7438	100.0	1404	4	US-10-622-373-2
2	7438	100.0	1404	5	US-10-756-149-5141
3	2084.5	28.0	838	4	US-10-622-373-6
4	1527.5	20.5	655	4	US-10-108-260A-3501
5	943	12.7	225	4	US-10-108-260A-2706
6	896	12.0	2338	4	US-10-029-386-31982
7	722.5	9.7	339	4	US-10-264-049-2738
8	720.5	9.7	574	5	US-10-450-763-38355
9	682.5	9.2	570	4	US-10-408-765A-1391
10	674.5	9.1	547	5	US-10-466-634-8
11	652.5	8.8	539	5	US-10-466-634-6
12	630.5	8.5	177	4	US-10-104-047-3332
13	630.5	8.5	177	6	US-11-072-512-3332
14	360	4.8	453	4	US-10-220-381-10
15	360	4.8	453	4	US-10-291-172-344
16	360	4.8	453	4	US-10-221-278-344
17	360	4.8	453	4	US-10-204-751A-3
18	349.5	4.7	379	3	US-09-729-674-4
19	349.5	4.7	379	5	US-10-913-553-4
20	345	4.6	337	3	US-09-780-996-9
21	345	4.6	337	4	US-10-726-721-9
22	345	4.6	342	4	US-10-408-765A-834
23	345	4.6	379	4	US-10-028-072-216
24	345	4.6	379	4	US-10-140-808-216
25	345	4.6	379	4	US-10-121-049-216
26	345	4.6	379	4	US-10-123-904-216
27	345	4.6	379	4	US-10-140-470-216
28	345	4.6	379	4	US-10-175-746-216
29	345	4.6	379	4	US-10-176-918-216
30	345	4.6	379	4	US-10-176-921-216
31	345	4.6	379	4	US-10-137-865-216

32	345	4.6	379	4	US-10-140-474-216	Sequence 216, App
33	345	4.6	379	4	US-10-142-431-216	Sequence 216, App
34	345	4.6	379	4	US-10-143-114-216	Sequence 216, App
35	345	4.6	379	4	US-10-142-419-216	Sequence 216, App
36	345	4.6	379	4	US-10-123-262-216	Sequence 216, App
37	345	4.6	379	4	US-10-142-423-216	Sequence 216, App
38	345	4.6	379	4	US-10-121-050-216	Sequence 216, App
39	345	4.6	379	4	US-10-141-755-216	Sequence 216, App
40	345	4.6	379	4	US-10-143-032-216	Sequence 216, App
41	345	4.6	379	4	US-10-123-108-216	Sequence 216, App
42	345	4.6	379	4	US-10-123-236-216	Sequence 216, App
43	345	4.6	379	4	US-10-123-261-216	Sequence 216, App
44	345	4.6	379	4	US-10-140-921-216	Sequence 216, App
45	345	4.6	379	4	US-10-140-928-216	Sequence 216, App

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:14:23 ; Search time 40 Seconds
(without alignments)
2348.683 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVVTCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1527.5	20.5	655	7	US-11-293-697-3501	Sequence 3501, Ap
2	943	12.7	225	7	US-11-293-697-2706	Sequence 2706, Ap
3	328.5	4.4	632	6	US-10-505-928-377	Sequence 377, App
4	302	4.1	323	7	US-11-354-653-87	Sequence 87, Appl
5	302	4.1	343	7	US-11-354-653-33	Sequence 33, Appl
6	292	3.9	308	7	US-11-354-653-136	Sequence 136, App
7	281.5	3.8	319	7	US-11-354-653-124	Sequence 124, App
8	281.5	3.8	354	7	US-11-354-653-127	Sequence 127, App
9	257	3.5	238	7	US-11-354-653-115	Sequence 115, App
10	211	2.8	1303	6	US-10-449-902-55274	Sequence 55274, A
11	195	2.6	674	7	US-11-040-219-2	Sequence 2, Appli
12	183	2.5	939	6	US-10-449-902-41543	Sequence 41543, A
13	175	2.4	1972	7	US-11-253-190-1	Sequence 1, Appli
14	171	2.3	1826	7	US-11-221-332-44	Sequence 44, Appl
15	166	2.2	509	6	US-10-449-902-38181	Sequence 38181, A
16	163	2.2	1614	6	US-10-505-928-199	Sequence 199, App
17	162.5	2.2	935	6	US-10-449-902-42274	Sequence 42274, A
18	161.5	2.2	284	7	US-11-354-653-121	Sequence 121, App
19	161	2.2	991	7	US-11-165-586-62	Sequence 62, Appl
20	160	2.2	738	6	US-10-953-349-5388	Sequence 5388, Ap
21	160	2.2	763	6	US-10-953-349-5387	Sequence 5387, Ap
22	158.5	2.1	3256	6	US-10-505-928-357	Sequence 357, App
23	157.5	2.1	1491	7	US-11-056-355B-101109	Sequence 101109,
24	157.5	2.1	1491	7	US-11-056-355B-112348	Sequence 112348,
25	157.5	2.1	1495	7	US-11-056-355B-101108	Sequence 101108,
26	157.5	2.1	1495	7	US-11-056-355B-112347	Sequence 112347,
27	156	2.1	1863	6	US-10-480-434A-16	Sequence 16, Appl
28	155	2.1	1251	6	US-10-953-349-8779	Sequence 8779, Ap
29	154.5	2.1	3934	7	US-11-165-586-20	Sequence 20, Appl

30	153	2.1	1263	6	US-10-540-898-539	Sequence 539, App
31	153	2.1	1466	7	US-11-056-355B-101110	Sequence 101110,
32	153	2.1	1466	7	US-11-056-355B-112349	Sequence 112349,
33	153	2.1	1498	7	US-11-266-446-94	Sequence 94, Appl
34	153	2.1	1828	7	US-11-056-355B-91730	Sequence 91730, A
35	153	2.1	1828	7	US-11-056-355B-95486	Sequence 95486, A
36	153	2.1	1999	7	US-11-056-355B-91729	Sequence 91729, A
37	153	2.1	1999	7	US-11-056-355B-95485	Sequence 95485, A
38	153	2.1	2008	7	US-11-056-355B-91728	Sequence 91728, A
39	153	2.1	2008	7	US-11-056-355B-95484	Sequence 95484, A
40	152	2.0	850	6	US-10-449-902-41508	Sequence 41508, A
41	151.5	2.0	584	7	US-11-293-697-4839	Sequence 4839, Ap
42	151	2.0	260	7	US-11-354-653-133	Sequence 133, App
43	151	2.0	295	7	US-11-354-653-130	Sequence 130, App
44	149.5	2.0	1032	6	US-10-449-902-45139	Sequence 45139, A
45	149	2.0	710	6	US-10-449-902-41319	Sequence 41319, A

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:06:57 ; Search time 53 Seconds
(without alignments)
2548.837 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFPVTCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7380	99.2	1395	2	T00068	hypothetical prote
2	360	4.8	453	2	JC7582	armadillo(arm) rep
3	342.5	4.6	1094	2	A53435	vesicular transpor
4	328.5	4.4	632	2	T00084	hypothetical prote
5	300	4.0	2550	2	B53435	vesicular transpor
6	284.5	3.8	5327	2	T13564	microtubule-associ
7	283.5	3.8	1110	2	I51116	NF-180 - sea lampr
8	252.5	3.4	1829	2	T24583	hypothetical prote
9	245	3.3	1805	2	A34736	nestin - rat
10	238.5	3.2	1804	2	T34518	nestin - golden ha
11	229	3.1	913	2	T52485	neurofilament prot
12	228	3.1	1871	2	D96796	probable heat shoc
13	220.5	3.0	1233	2	S56271	hypothetical prote
14	217.5	2.9	1052	1	A44937	kinetoplast-associ
15	210.5	2.8	3488	2	T34418	hypothetical prote
16	210	2.8	1132	2	T43483	translation initia
17	206	2.8	4574	2	G02520	plectin - human
18	202	2.7	1618	2	S21424	nestin - human
19	198.5	2.7	1403	2	T11583	probable translati
20	198	2.7	2261	2	T20978	hypothetical prote
21	197.5	2.7	837	2	JN0292	antigen 332 - mala
22	197.5	2.7	1567	2	T03730	antigen containing
23	197.5	2.7	2241	2	T20971	hypothetical prote
24	196.5	2.6	4687	1	A39638	plectin - rat
25	196	2.6	1526	2	A45605	mature-parasite-in
26	195	2.6	4684	2	A59404	plectin [imported]
27	193.5	2.6	1684	2	JW0057	gravin - human
28	193.5	2.6	4385	2	T29042	hypothetical prote
29	193	2.6	2364	2	A56577	microtubule-associ
30	192	2.6	5170	2	T15348	hypothetical prote
31	190.5	2.6	1020	1	QFHUH	neurofilament trip
32	190	2.6	1621	2	A82255	hypothetical prote
33	189.5	2.5	2774	2	A43359	microtubule-associ

34	188	2.5	3924	2	S37431	ankyrin 2, neurona
35	186	2.5	6642	2	T29757	protein UNC-89 - C
36	185.5	2.5	2464	1	QRMSF1	microtubule-associ
37	184.5	2.5	1641	2	I38614	helicase II - huma
38	183.5	2.5	2484	2	T26216	hypothetical prote
39	183.5	2.5	2607	2	T26215	hypothetical prote
40	183	2.5	407	1	EDBEQ3	immediate-early pr
41	181	2.4	1346	2	A57376	probable regulator
42	180.5	2.4	721	2	S29795	hypothetical prote
43	180.5	2.4	793	1	JH0628	caldesmon - human
44	180	2.4	839	2	E84824	hypothetical prote
45	180	2.4	1589	2	C44766	defective chorion-

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:03:02 ; Search time 335 Seconds
(without alignments)
3876.782 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVTCMTGTAEIESGAQ.....AKELGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	7437	99.9	1404	2	O43168_HUMAN
2	7373	99.1	1395	2	Q5JY77_HUMAN
3	4045	54.4	1350	2	Q8CHF4_MOUSE
4	4029	54.2	1347	2	Q5U4C1_MOUSE
5	3976.5	53.5	1346	2	Q920R4_RAT
6	2721.5	36.6	874	2	Q8R095_MOUSE
7	2567.5	34.5	957	2	Q6PD32_MOUSE
8	2093.5	28.1	838	2	Q5R7U0_PONPY
9	2084.5	28.0	838	2	Q96D09_HUMAN
10	1527.5	20.5	655	2	Q8N8W9_HUMAN
11	1495.5	20.1	405	2	Q8BYK9_MOUSE
12	1044	14.0	379	2	Q8BKR8_MOUSE
13	961	12.9	347	2	Q8BUN4_MOUSE
14	757.5	10.2	995	2	Q8K2R3_MOUSE
15	682.5	9.2	570	2	Q9C0G2_HUMAN
16	674.5	9.1	547	2	Q6PI77_HUMAN
17	674.5	9.1	547	2	Q9BE11_MACFA
18	652.5	8.8	539	2	Q71HP2_RAT
19	631.5	8.5	352	2	Q8BUY8_MOUSE
20	630.5	8.5	177	2	Q8NAB4_HUMAN
21	629.5	8.5	539	2	Q6PB60_MOUSE
22	550.5	7.4	558	1	ARMX5_HUMAN
23	539	7.2	606	1	ARMX5_MOUSE
24	536.5	7.2	558	1	ARMX5_PONPY
25	521	7.0	497	2	Q8R0B3_MOUSE
26	475	6.4	342	2	Q5H9K7_HUMAN
27	431	5.8	340	2	Q8R103_MOUSE
28	378.5	5.1	2197	2	Q57TX7_TRYYP
29	360	4.8	453	1	ARMX1_HUMAN
30	355	4.8	360	2	Q69ZD0_MOUSE
31	350.5	4.7	461	1	ARMX1_RAT
32	350	4.7	453	1	ARMX1_PONPY
33	346	4.7	456	1	ARMX1_MOUSE
34	345	4.6	379	1	ARMX3_HUMAN
35	345	4.6	379	1	ARMX3_PONPY

36	342.5	4.6	1094	2	Q26774_9TRYP	Q26774 trypanosoma
37	341	4.6	379	1	ARMX3_MOUSE	Q8bhs6 mus musculu
38	341	4.6	379	1	ARMX3_RAT	Q5xid7 rattus norv
39	328.5	4.4	632	1	ARMX2_HUMAN	Q71311 homo sapien
40	324.5	4.4	624	2	Q5RfK2_PONPY	Q5rfk2 pongo pygma
41	320	4.3	2316	1	UAFA_STAS1	Q4a0v8 staphylococ
42	310	4.2	306	2	Q9CZ87_MOUSE	Q9cz87 mus musculu
43	310	4.2	306	2	Q9D0L7_MOUSE	Q9d017 mus musculu
44	310	4.2	1209	2	Q3XRG5_9PROT	Q3xrg5 magnetococc
45	307	4.1	308	2	Q9BTM6_HUMAN	Q9btm6 homo sapien